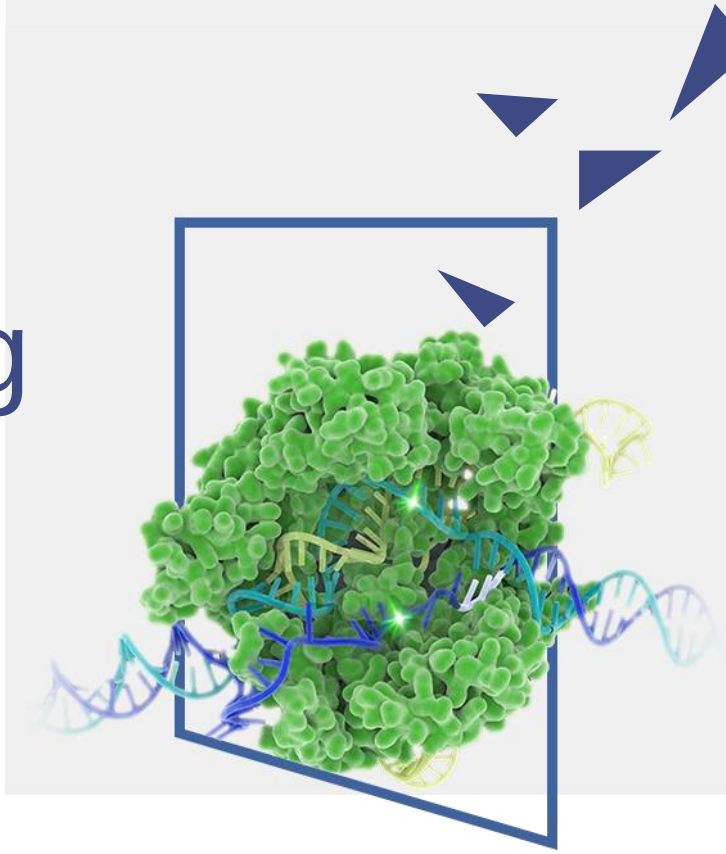
CD Genomics
The Genomics Services Company

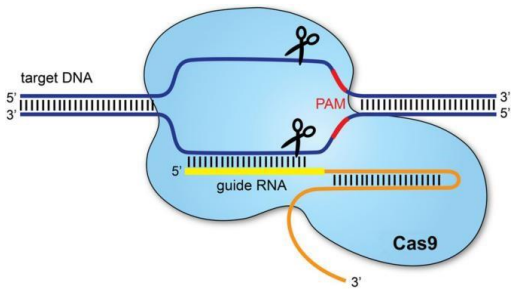
CRISPR Sequencing



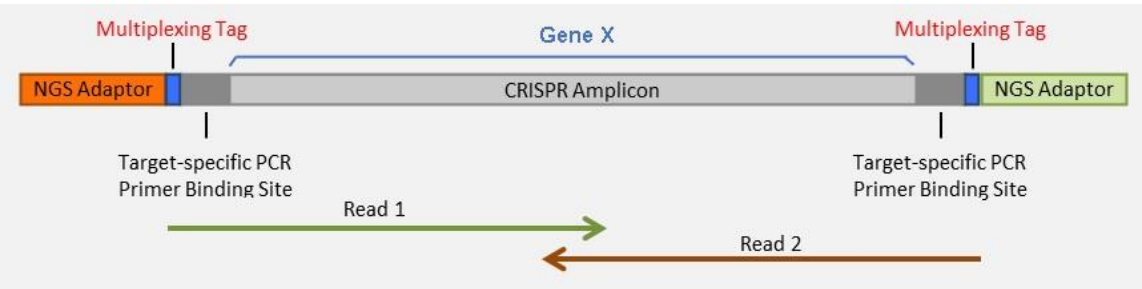
CD Genomics is a world leading Genomics Services Company that innovates sequencing, genotyping, microarray, bioinformatics, and microbiome studies for academics, pharmaceuticals, biotechnologies, and health facilities. CD Genomics has developed the CRISPR sequencing platform based on our deep understanding of CRISPR/Cas9 genome editing technology and genomics expertise. With our CRIPSR sequencing service, you are able to validate gRNA libraries and genome editing in a both high-throughput and accurate manner.

Why Do You Need CRISPR Sequencing?

The CRISPR-Cas9 gene targeting system is a simple, versatile, precise, and effective method of genetic manipulation that has many potential applications such as medicine and crop seed enhancement. Validating edits is especially important in the CRISPR experimental process since off-target mutation and not an edit in the target gene could happen. Another issue of CRISPR technology is the occurrence of Off-target cuts. The CRISPR system cut not just at its target place, but also at unintended sites with similar sequences. Our CRISPR sequencing service can help you with these issues to create perfect genome edits.



Principle of CRISPR Sequencing Technology



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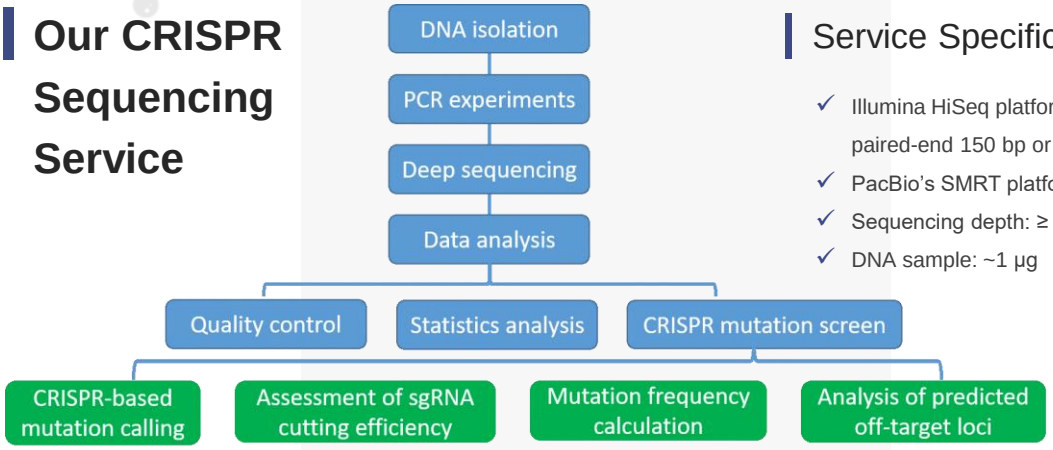
Our High-throughput CRISPR sequencing is based on the principle of targeted amplicon sequencing by conducting PCR experiments using primers flanking the target region. Targeted amplicon sequencing is the most sensitive method for checking mutations and the detection frequencies are as low as 0.01%. The site of interest is amplified with target-specific PCR primers, which are then sequenced by NGS platforms after adding both NGS adaptors and a unique barcode. We also apply software tools to predict off-target effects of sgRNAs and pinpoint the location of possible mismatches across the genome, as larger mismatches (e.g. six nucleotides) may cause off-target double-stranded breaks (DSBs).

Our CRISPR Sequencing Service



Service Specification

- ✓ Illumina HiSeq platforms, paired-end 150 bp or 300 bp;
- ✓ PacBio's SMRT platform
- ✓ Sequencing depth: ≥ 1000x
- ✓ DNA sample: ~1 μg

Sample requirements

- ✓ Samples types: cell or DNA samples after CRISPR-Cas gene editing manipulation
- ✓ DNA sample: ~1 μg (concentration ≥ 30 ng/μl; OD260/280=1.8~2.0)
- ✓ Cell sample: 1×106 cells or 10 cm2 cell culture

Bioinformatics Analysis

- ✓ Raw data QC
- ✓ Reference alignment
- ✓ Validation of CRISPR libraries
- ✓ Analysis of target loci
- ✓ Analysis of predicted off-target loci

Applications

- ✓ Verify your guide library
- ✓ Validate CRISPR/Cas9 targets and mutation efficiency
- ✓ Discover the candidates with most impact from screenings and the frequency and implications of the edits

Features

- ✓ Extensive multiplexing flexibility and high-throughput sequencing, up to 10^4 samples per run
- ✓ Ultra-deep sequencing of amplicons or captured regions, in excess of 1000X coverage
- ✓ Cost-effective, and highly sensitive detection levels without bias
- ✓ No need for laborious and time-consuming cloning steps

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Contact Us

Contact CD Genomics for more inspiration and service content.